

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: September 18, 2006, 00:41:40 ; Search time 4618 Seconds
(without alignments)
7156.415 Million cell updates/sec

Title: US-10-733-816-2
Perfect score: 2081
Sequence: 1 MEYNPMEGGMGSRPTTSF.....QELSSNPPLATILIPPHARI 394

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 48236798 seqs, 27959665780 residues
Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=framet p2n.model -DEV=exp
-Q=/abs/ABSSWEB_spool/US10733816/runat_15092006.085446.15519/app.query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=10 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03p
-USER=US10733816 ACGN_1.1.9528 @runat_15092006.085446.15519 -NCPU=6 -ICPU=3
-NO_MAP -NEG_SCORES=0 -WAIT -DISPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1.*
2: gb_est3.*
3: gb_est4.*
4: gb_est5.*
5: gb_est6.*
6: gb_hic.*
7: gb_est2.*
8: gb_est7.*
9: gb_est8.*
10: gb_est9.*
11: gb_gss1.*
12: gb_gss2.*
13: gb_gss3.*
14: gb_gss4.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2015	96.8	2312	6 AK170965	AK170965 Mus muscu
2	2013	96.8	2847	6 AK154293	AK154293 Mus muscu
3	2013	96.7	1732	6 CR617019	CR617019 full-leng
4	1609	77.3	1897	6 CR610570	CR610570 full-leng
5	1609	77.3	2119	6 CR615336	CR615336 full-leng
6	1609	77.3	2124	6 CR593340	CR593340 full-leng
7	1594	76.6	1760	6 CR597295	CR597295 full-leng
8	1594	76.6	3536	6 CR749620	CR749620 Homo sapi
9	1556	74.8	1094	10 W18183	W18183 IMAGE:20087
10	1446	69.5	841	9 CX795595	CX795595 JGI_CAAJ1
c 11	1415	68.0	818	9 DN530922	DN530922 1386786 M
12	1410.5	67.8	993	8 CO579074	CO579074 ILLUMIGEN
13	1403	67.4	869	10 DT309300	DT309300 JGI_CAAJ1
14	1387	66.7	2190	6 AK164048	AK164048 Mus muscu
15	1379	66.3	890	3 BQ651422	BQ651422 AGENCOURT
16	1368	65.7	844	10 DV929624	DV929624 LB03017.C
17	1362.5	65.5	931	1 AL536089	AL536089 AL536089
c 18	1336	64.2	946	1 AL521664	AL521664 AL521664
19	1334.5	64.1	930	3 BQ651351	BQ651351 AGENCOURT
c 20	1333	64.1	935	4 CA976264	CA976264 AGENCOURT
21	1318.5	63.4	1094	2 BM478839	BM478839 AGENCOURT
22	1317	63.3	774	4 CB465245	CB465245 726514 MA
23	1316	63.2	812	8 CV557169	CV557169 UI-M-H20-
24	1315	63.2	863	10 DT280981	DT280981 JGI_CAAV9
25	1312	63.0	749	4 CB450430	CB450430 705088 MA
26	1308	62.9	886	3 BQ654247	BQ654247 AGENCOURT
27	1296	62.3	747	2 BI558388	BI558388 603240449
28	1291	62.0	800	10 DT154092	DT154092 JGI_ANN03
29	1268	60.9	889	3 BQ673346	BQ673346 AGENCOURT
30	1266	60.8	927	3 BQ669839	BQ669839 AGENCOURT
31	1263.5	60.7	1275	13 CL963186	CL963186 OsIFCC008
32	1259	60.5	1745	6 AY106255	AY106255 Zea mays
33	1257.5	60.4	1752	6 AY108486	AY108486 Zea mays
34	1256	60.4	785	5 CK468065	CK468065 939430 MA
35	1255	60.3	781	10 DV907419	DV907419 LB0282.CR
36	1253.5	60.2	1197	13 CL957492	CL957492 OsIFCC000
37	1247	59.9	1967	6 AY103545	AY103545 Zea mays
c 38	1245	59.8	785	5 CK465964	CK465964 937126 MA
39	1240.5	59.6	755	2 BG210727	BG210727 RST30273
40	1233	59.3	1666	6 AY104068	AY104068 Zea mays
41	1232	59.2	1409	6 CNSOAB1V	BX815323 Arabidops
42	1232	59.2	1461	6 CNSOAB1V	BX817800 Arabidops
43	1231	59.2	1711	6 DQ241848	DQ241848 Solanum t
44	1228	59.0	1593	6 DQ252508	DQ252508 Solanum t
45	1225	58.9	1638	6 CNS09YXF	BX831446 Arabidops

ALIGNMENTS

RESULT 1
AK170965
LOCUS
DEFINITION Mus musculus NOD-derived Cd11c +ve dendritic cells cDNA, RIKEN
2312 bp mRNA linear HTC 21-SEP-2005

full-length enriched library, clone: F630213P21 product: glycogen
synthase kinase 3 beta, full insert sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AK170965
AK170965.1 GI:74221330

HTC; CAP trapper.
Mus musculus (house mouse)

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Mus.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-Format
sequencing pipeline with 384 multichannel sequencer

Genome Res. 10 (11), 1757-1771 (2000)

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
Kadota, K., Matsumura, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuenli, P., Lewis, S., Matsuo, Y., Nika, I., Nika, I., Pesole, G.,
Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H.,
Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S.
and Hayashizaki, Y.

RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

11217851

5

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Ooato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

FANTOM Consortium

CONSRM

TITLE

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420 (6915), 563-573 (2002)

12466951

6

Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C.,
Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R.,
Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R.,
Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E.,
Ambesi-Impombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L.,
Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M.,
Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R.,
Crome, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G.,
di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Faulkner, G.,
Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M.,
Georgii-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E.,
Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N.,
Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T.,
Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kelso, J., Kitamura, H.,
Kitano, H., Kollias, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K.,
Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J.,
Liu, S., McWilliam, S., Madan, B., Madera, M., Marchionni, L.,
Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S.,
Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H.,
Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O.,
Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavoni, G.,
Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.F., Ring, B.Z.,
Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A.,
Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S.,
Sessa, L., Sheng, Y., Shibata, Y., Shimada, K., Shimada, K., Silva, D.,
Sincic, B., Sperling, S., Stupka, E., Sugliura, K., Sulcane, R.,
Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S.,
Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R.,
Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A.,

	1.08e-210	Length:	2312
	2015.00	Matches:	386
	98.0%	Conservative:	0
:	98.0%	Mismatches:	2
	96.8%	Indels:	6
	6	Gaps:	1

US-10-733-816-2 (1-394) x AK170965 (1-2312)

7	GLUGlyGlyGly:-----MetSerGlyArgProArgThrThrSerPhe	20
943	GAAGGAAAGGTGATTCAAGAGAGCCATCATGTCGGGGCCACCGAGAACCACTCTTT	1002
21	AlaGluSerCysIysProValGlnProSerAlaPheGlySerMetLysValSerArg	40
1003	CGCGAGAGCTGCAGCCAGTSCAGCAGCCTTCAGCTTTTGATGACCAAGTTATGACAGA	1062
41	AspLysAspGlySerIysValThrThrValValAlaThrProGlyGlnGlyProAspArg	60

DB 1063 GATAAAGATGGCAGCAAGGTAAACACAGTAGTGGCAACTCCTGGCCAGGGTCCCTGACAGG 1122

61 PROGINUVALSERLYRINRASPINRLYGVATIEGLYASNGLYSEIFNEGLYVAL 80

UD CCACAGGAAGTCAGTATATACAGACACGAAAGTGATGGATAAGATCATTTGGGTGGTA 1102

01 1YGRIMRATYSTREUCYSKSPCEU7YGRUUCUVAIRARCEU73U7EVAIRUCORIMSP 100

[illegible]

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

Hide W. Bult, C. Grummond S.M., Teasdale R.D., Liu E.T.
Braulic, V., Quackenbush, J., Wahlstedt C., Mattick, J.S., Hume, D.A.,
Kai C.S., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M.,
Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Icon, M.,
Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M.,
Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M.,
Plessley, C., Shiraki, T., Suzuki, S., Tagami, M., Waki, K.,
Watanahiki, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
FANTOM Consortium

The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)

7
Katayama S., Tomaru Y., Kasukawa T., Waki K., Nakanishi M., Nakamura M., Hayashida H., Yap C.C., Suzuki M., Kawai J., Suzuki H., Gernini P., Henrichzaki Y., Wells C., Frith M., Ravasi T., Chang K.C., Hallinan J., Matlick J., Hume D.A., Lipovich L., Stakalov S., Engstrom, P.G., Mizuno, Y., Faghini M.A., Sandelin, A., Chalk A.M., Mottagui-Tabar, S., Liang Z., Lenhard B. and Weststedt, C.

RIKEN Genome Exploration Research Group
Antisense transcription in the mammalian transcriptome
Science 309 (5740): 1564-1566 (2005)

8 (pages 1 to 2312)

Karakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Horii, F., Iida, Y., Inamura, K., Imotani, K., Itoh, M., Kanegawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishikiori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Watanuki, A., Watanabe, K., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), 1-7-2 Sushiro-cho, Tsukumi-ku, Yokohama, 230-0045, Japan (E-mail: genomo-re@gsc.riken.jp, [URL: http://www.gsc.riken.jp/](http://www.gsc.riken.jp/), Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. The Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/WRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

```
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers
1. 2312
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="FANTOM_DB:F630213P21"
/db_xref="taxon:10090"
/cclone="F630213P21"
/cell_type="NOD-derived CD11c +ve dendritic cells"
/clong_lib="RIKEN full-length enriched mouse cDNA library"
```

PERSONAL - Nennen Sie einen Einflussfaktor beim Prozess / Personal_200 - Nennen Sie einen Einflussfaktor beim Prozess

QY	181	TyrileHisSerPheGlyLeCysHisArgAspIleLysProGlnAsnLeuLeuAsp	200
DB	1483	TATATCATCTCTTTGGAACTTCCTCCAGACATTAACACACAGACCTCTTGTTGGAT	1542
QY	201	ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly	220
DB	1543	CCTGATACAGCTGTATTAAACTCTGACTTTGGAAGTGCAAGACAGCTGTGTCGAGGA	1602
QY	221	GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly	240
DB	1603	GAGCCCAATCTTTCATATATCTCTCGTACTACAGGACCACAGAGTTGATCTTTGGA	1662
QY	241	AlaThrAspTyrThrSerIleAspValTyrSerAlaGlyCysValLeuAlaGluLeu	260
DB	1663	GCCACTGATTACACATCCAGTATAGATGTGTGCTCGAGGCTGTGTGGCTGAATG	1722
QY	261	LeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIle	280
DB	1723	TGCTAGACACACCAATATTTCTCGGGACAGTGTGTGTGATCAGTTGTGGAAATATA	1782
QY	281	LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu	300
DB	1783	RAGTCTAGAACACCAACAGGAGCAATTAGAGAAATGACCAATATATACAGAA	1842
QY	301	PheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrPro	320
DB	1843	TTCAATTCCTCAATCAAGGCACATCTTGGCAAGAGTCTTCGGGCCCAACTCCA	1902
QY	321	ProGluAlaIleAlaLeuLysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr	340
DB	1903	CCAGAGGCAATGTGCACTGTGACCGCTCTGTGGAGTACACACCTACCGCCCGCTACA	1962
QY	341	ProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLysHis	360
DB	1963	CCACTGGAACTTGTGCATCTCATTTCGATGAATTCGGGACCCCAATGTCAAACTA	2022
QY	361	ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn	380
DB	2023	CCAAATGGCGAGACACACCTGCACCTCTTCAACTTTTACCACCTCAAGAACTGTCAAGTAAC	2082
QY	381	ProProLeuAlaThrIleLeuIleProProHisAlaArgIle	394
DB	2083	CCCCCTCGCCACCACCTCTTATCCCTCCACATCTCGGATT	2124
RESULT 2			
AK154293		2847 bp mRNA linear HTC 21-SEP-2005	
LOCUS		Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN	
DEFINITION		full-length enriched library, clone:F630015J08 product:glycogen	
		synthase kinase 3 beta, full insert sequence.	
ACCESSION		AK154293	
VERSION		AK154293.1 GI:74178475	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;	
		Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE		1	
AUTHORS		Carninci, P. and Hayashizaki, Y.	

TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayateu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, F., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.
CONSRMT	RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
PUBMED	11217851
REFERENCE	5
AUTHORS	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V., Choithia, C., Corbani, L. E., Cousins, S., Della, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

REFERENCE	7	Numata, K., Okido, T., Pavan, W. J., Perteau, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Uetani, K., Wagner, L., Wahlestedt, C., Wang, X., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, L., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A. C., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, E., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
CONSTRM		PANTOM Consortium
TITLE		Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL		Nature 420 (6915), 563-573 (2002)
PUBMED		12466851
REFERENCE	6	Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M. C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzius, R., Shimokawa, K., Bajic, V. B., Brenner, S. E., Batalov, S., Forrest, A. R., Zavolan, M., Davis, M. J., Wilming, L. G., Aidinis, V., Allen, J. E., Ambesi-Impombato, A., Apweiler, R., Aturaliya, R. N., Bailey, T. L., Bansal, M., Baxter, L., Beisel, K. W., Bersano, T., Bono, H., Chalk, A. M., Chiu, K. P., Choudhary, V., Christoffels, A., Clutterbuck, D. R., Cowie, M. L., Dalla, E., Dalrymple, B. P., de Bono, B., Della Gatta, G., di Bernardo, D., Down, T., Engstrom, P., Fagioli, M., Faulkner, G., Fletcher, C. F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgii-Hemming, P., Gingeras, T. R., Gojobori, T., Green, R. E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T. K., Hirokawa, N., Hill, D., Huminec, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jakt, M., Kanapin, A., Katoh, M., Kawasawa, Y., Kello, J., Kitamura, H., Kitano, H., Kollas, G., Kriehnan, S. P., Kruger, A., Kummerfeld, S. K., Kurochkin, I. V., Larau, L. F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, B., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K. C., Pavan, W. J., Pavesi, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J. F., Ring, B. Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S. L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C. A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugura, K., Sultana, R., Takenaka, Y., Taki, K., Tanno, J. K., Tan, S. L., Tang, S., Taylor, M. S., Tegner, J., Teichmann, S. A., Ueda, H. R., van Nimwegen, E., Verardo, R., Wei, C. L., Yagi, K., Yamashita, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimmond, S. M., Teasdale, R. D., Liu, E. T., Brusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J. S., Hume, D. A., Kai, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori-Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Ohashi, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wachihi, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
CONSTRM		PANTOM Consortium
TITLE		The transcriptional landscape of the mammalian genome
JOURNAL		Science 309 (5740), 1559-1563 (2005)
PUBMED		16141072
REFERENCE	7	Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C. C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Pang, K. C., Hallinan, J., Mattick, J., Hume, D. A., Lipovich, L., Batalov, S., Engstrom, P. G., Mizuno, Y., Faghihi, M. A., Sandelin, A., Chalk, A. M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
CONSTRM		RIKEN Genome Exploration Research Group
TITLE		Antisense transcription in the mammalian transcriptome
JOURNAL		Science 309 (5740), 1564-1566 (2005)
PUBMED		16141073
REFERENCE	8	(bases 1 to 2847)
AUTHORS		Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wachihi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE		Direct Submission
JOURNAL		Submitted (30-MAR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT		cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
FEATURES		Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
source		Please visit our web site for further details.
		URL: http://genome.gsc.riken.jp/
		URL: http://fantom.gsc.riken.jp/
		Location/Qualifiers
	1..2847	
	/organism="Mus musculus"	
	/mol_type="mRNA"	
	/strain="NOD"	
	/db_xref="FANTOM DB:F630015J08"	
	/db_xref="taxon:10090"	
	/clone="F630015J08"	
	/cclone_type="NOD-derived CD11c +ve dendritic cells"	
	/clone_lib="RIKEN full-length enriched mouse cDNA library"	
	1004..2266	
	/note="unnamed protein product; glycogen synthase kinase 3 beta (MGD MG1.1861437 GB NM_019827, evidence: BLASTN, 99%, match=2350)	
	putative"	
	/codon_start=1	
	/protein_id="BAE32494.1"	
	/db_xref="GI:74178476"	
	/translation="MSGRRPTTSFAESCSPVQPSAFGSMKVSBDKSGKVTTVVAFPGQGPDPQEVSTDTKTVIGNSGFGVQAKLDSGLVAIKKVLQKRRFKREIQ.I.MRKLDPKCNIVRLFFYSGSGKDEVJLNLVDYVPETVYRVARHYSKQTLFVYVKLYMYQLFRSLAYIHSFGICHDRIDIKPNLLDPDTAVLKLCDFGSAKQVGRGPNVSYIC	

SRYYRAPELIFGATDYTSIDWSAGCVLAELLGQIFPFQDSGVOLVBIKVLGTP
TREQIREWNNYTERKFKPQIKAHKPTKVPRTPEALALCSLLEYTPFARLTPLA
CAHSFDELDPNWKLPNGRDTPALFNFTQELSSNPPLATILIPPHARIOAAASPPA

Alignment Scores:

Pred. No.: 1,47e-210 Length: 2847
Score: 2015.00 Matches: 386
Percent Similarity: 98.0% Conservative: 0
Best Local Similarity: 98.0% Mismatches: 2
Query Match: 96.8% Indels: 6
DB: Gaps: 1

US-10-733-816-2 (1-394) x AK154293 (1-2847)

QY	7	GlulGlyGlyCly-----MetSerClyArgProArgThrThrSerPhe	20
DB	974	GAAGGAAAGGTGATTCAAGAGAGCCATCATGTGCGGGCGACCGAGAACCCCTCTTT	1033
QY	21	AlaGluSerCysAlaProValGlnGlnProSerAlaPheGlySerMetLysValSerArg	40
DB	1034	CGCGAGAGCTGCAACGCCAGTCGACAGCCCTTCAGCTTTTGGTAGCATGAAGTTAGCAGA	1093
QY	41	AspLysAspGlySerLysValThrValValAlaThrProGlyGlnGlyProAspArg	60
DB	1094	GATTAAGATGGCAGCAGGTAAACACAGTAGTGGCAACTCTCTGCCAGGGTCTCGACAGG	1153
QY	61	ProGlnGluValSerThrAspThrLysValIleGlyAsnGlySerPheGlyValVal	80
DB	1154	CCACAGGAGTCACTTATACAGACACGAAAGTGATTGGAAATGGATCAATTTGGTGGTA	1213
QY	81	TyrGlnAlaLysCysAspSerGlyGluLeuValAlaIleLysLysValLeuGlnAsp	100
DB	1214	TATCAAGCCAACTTTGTGATTCTGGAGAACTGGTTGCCATCAAGAAAGTTCTACAGGAC	1273
QY	101	LysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIleVal	120
DB	1274	AAGCGATTAAAGAACCGAGAGCTCCAGATCATGAGAAAGCTAGACCACTGTACATAGTC	1333
QY	121	ArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsnLeu	140
DB	1334	CGACTGGGTATTTCTTACTACTGCTGCGAGGAGAAAGATGAGTCTTACCTTAACCTG	1393
QY	141	ValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaLys	160
DB	1394	GTGCTGCACTATGTTCCGAGACAGTGTACAGAGTCCAGACACTATAGTCGAGCAG	1453
QY	161	GlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAla	180
DB	1454	CAGACACTCCCTGTGATCTATGTCAAGTTGTATATGTATCATGCTGTTTCAGAACTCTAGCC	1513
QY	181	TyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAsp	200
DB	1514	TATATCAATCTCTTTGGAAATCTGCCATCGACATTAACCCACAGACCTCTTTGTGGAT	1573
QY	201	ProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGly	220
DB	1574	CCTGATACAGCTGATTAAACTCTGACTTTGGAAGTGAACAGCAGCTGGTCCGAGGA	1633
QY	221	GluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGly	240
DB	1634	GAGGCCAAATGTTTCATATATCTGTCGTACTACAGGCCACAGAGTGTATCTTTCGA	1693

QY	241	alaThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeu	260
DB	1694	GCCACTGATTACACGTCAGTATGATGTATGGTCTGCAGGCTGTGTGTGGCTGAATTG	1753
QY	261	LeuLeuGlyGlnProIlePhePheProGlyAspSerGlyValAspGlnLeuValGluIle	280
DB	1754	TTGCTAGACACCAATATTTCTGGGACAGTGTGTGGATCAGTGTGTGGAAATATA	1813
QY	281	LysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGlu	300
DB	1814	AAGGTCTAGAACACCAACAGGAGCAAAATTAGAGAAATGAAACCAATTATACAGA	1873
QY	301	PheLysPheProGlnIleLysAlaHisProTrpThrLysValPheArgProArgThrPro	320
DB	1874	TTCAAAATTCCTCAATCAAGGCACATCTTTGGCAAAAGTCTTCGGCCCCCAACTCA	1933
QY	321	ProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeuThr	340
DB	1934	CCAGAGCAATGCACTGTGACGCGCTGTGTGGGTACACACTTCCGCGCCGGCTTACA	1993
QY	341	ProLeuGluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHis	360
DB	1994	CCACTGGAAGCTTGTGCACATTCATTTTTCGATGAATGGGGACCCCAATGTCAAACTA	2053
QY	361	ProAsnGlyArgAspThrProAlaLeuPheAsnPheThrThrGlnGluLeuSerSerAsn	380
DB	2054	CCAAATGGCGAGACACACTTGCACCTCTTCAACTTTTACCACCTCAAGAACTGTCAAGTAA	2113
QY	381	ProProLeuAlaThrIleLeuIleProProHisAlaArgIle	394
DB	2114	CCCCCTTGGCCACCACCTCTTATCCCTCCACATCTCGGATT	2155

RESULT 3

LOCUS CR617019 1732 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DB003YJ02 of Neuroblastoma Cot
10-normalized of Homo sapiens (human).

ACCESSION CR617019
VERSION CR617019.1 GI:50497826
KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1 (bases 1 to 1732)
AUTHORS Li.W.B., Gruber,C., Jesse,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue

REFERENCE 2 (bases 1 to 1732)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

FEATURES

Location/Qualifiers

source 1..1732
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS008003YJ02"
 /tissue_type="Neuroblastoma Cot 10-normalized"
 /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 1.18e-210 Length: 1732
 Score: 2013.00 Matches: 383
 Percent Similarity: 99.7% Conservative: 0
 Best Local Similarity: 99.7% Mismatches: 1
 Query Match: 96.7% Indels: 0
 DB: 6 Gaps: 0

US-10-733-816-2 (1-394) x CR617019 (1-1732)

QY 11 MetSerGlyArgProArgThrThrSerPheAlaGluSerCysLysProValGlnGlnPro 30
 DB 395 ATGTCAGGCGCGCCAGAACCACTCTCTTGGGAGAGCTGCAACCGGTGCAGCAGCT 454
 QY 31 SerAlaPheGlySerMetLysValSerArgAspLysAspGlySerLysValThrVal 50
 DB 455 TCACGCTTTGGCAGCATCAAGTTACGACAGACAAAGCGGCGCAGGTTGACACACGTG 514
 QY 51 ValAlaThrProGlyGlnGlyProAspArgProGlnGlnValSerThrAspThrLys 70
 DB 515 GTGGCAACTCTCTGGCAGGTCACAGACAGGCGCACAGAGTCAAGTCAAGTCAAGTCA 574
 QY 71 ValIleGlyAsnGlySerPheGlyValValThrGlnAlaLysLeuCysAspSerGlyGlu 90
 DB 575 GTGATTGGAAATGGATCATTTGGTGTGTATATCAAGCCCAAACTTTGTGATTCAAGGAA 634
 QY 91 LeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnTle 110
 DB 635 CTGTGCCCATCAAGAAAGTATTGCGAGCAAGAGATTATAGATCGAGAGCTCCAGATC 694
 QY 111 MetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGly 130
 DB 695 ATGAGAAAGCTAGATCACTGTACATAGTCGATTCGGATTGGTATTCTTCTACTCCAGTGT 754
 QY 131 GluLysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyr 150
 DB 755 GAGAAGAAGATGAGTCTATCTTAATCTGGTGTGCTGACTATGTTCCGAAACAGTATAC 814
 QY 151 ArgValAlaAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeu 170
 DB 815 AGAGTTCCAGACACTATAGTCGAGGCAACAGACGCTCCCTGTGATTATGTCAGATTG 874
 QY 171 TyrMetTyrGlnLeuPheAspSerLeuAlaTyrIleHisSerPheGlyIleCysHisArg 190
 DB 875 TATATGATACGCTGTTCGGAAGTTTAGCTATATATCATTCCTTTTGGATCTCCATCG 934
 QY 191 AspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAsp 210

DB 935 GATATTAAACCCGACAGACCTCTTTGGAGTCTGTACTACTCTGTATTAAACCTCTGTGAC 994
 QY 211 PheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArg 230
 DB 995 TTTGGAAGTGCAGACAGCTGGTCCGAGGAGAACCCCAATGTTTCGTATATCTGTTCTGG 1054
 QY 231 TyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspVal 250
 DB 1055 TACTATAGGCGCAGAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTAGATGTA 1114
 QY 251 TrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAsp 270
 DB 1115 TGGTCTGCTGGCTGTGTGTGGCTGAGCTGTTACTAGGACCAACCAATATTTCCAGGGGAT 1174
 QY 271 SerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGln 290
 DB 1175 AGTGTGTGGATCAGTTGGTAGAAATAATCAAGGTCTCTGGAACTCCCAACAGGAGCAA 1234
 QY 291 IleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisPro 310
 DB 1235 ATCAGAGAAATGAACCCAACTACACAGAAATTTAAATTCCTCAATATTAGGCACATCT 1294
 QY 311 TrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCysSerArgLeu 330
 DB 1295 TGGACTAAGTCTTCGACCCCGAACTCCACGCGAGGCAATTGCACTGTGTAGCCCTCTG 1354
 QY 331 LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe 350
 DB 1355 CTGGAGTATACCAACTGCCCGCACTAACCACTTGAAGCTTGTGCACATTCATTTT 1414
 QY 351 AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe 370
 DB 1415 GATCAATTTACGGACCCCAATGTCAAACTACCAAACTGGCGAGACACACCTGTGACTTTC 1474
 QY 371 AsnPheThrThrGlnLeuSerSerAsnProProLeuAlaThrIleLeuLeuProPro 390
 DB 1475 AACTTCACCACTCAAGAACTGTCAAGTAATCCACTCTGCTACCATCTTATTTCTCTCT 1534
 QY 391 HisAlaArgile 394
 DB 1535 CATGCTCGGATT 1546

RESULT 4
 CR610570
 LOCUS 1897 bp mRNA linear HTC 21-JUL-2004
 DEFINITION full-length cDNA clone CS0DJ012YC04 of T cells (Jurkat cell line)
 Cot 10-normalized of Homo sapiens (human).
 CR610570
 ACCESSION CR610570.1 GI:50491377
 VERSION HTC; CNSUT_CDNA.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Homo.
 REFERENCE 1 (bases 1 to 1897)
 AUTHORS Li W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 CONTACT Contact : Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

REFERENCE Paraday Avenue
 2 (bases 1 to 1897)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
 BP 191, 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen.
 FEATURES
 source Location/Qualifiers
 1..1897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODJ012YC04"
 /tissue_type="T cells (Jurkat cell line) Cot
 10-normalized"
 /plasmid="pCMVSPORT_6"
 ORIGIN
 Alignment Scores:
 Pred. No.: 5,52e-166 Length: 1897
 Score: 1609.00 Matches: 319
 Percent Similarity: 77.3% Conservative: 24
 Best Local Similarity: 71.8% Mismatches: 43
 Query Match: 77.3% Indels: 58
 DB: 6 Gaps: 4
 US-10-733-816-2 (1-394) x CR610570 (1-1897)
 QY 5 ProMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
 DB 176 CCTTCGGGAGGCGCCCTGGGGGCTCGGCGAGGCGCGACTAGCTGTTCCGGAG--- 232
 QY 24 CysLysPro-----ValGlnGln 29
 DB 233 -----CCCGCGCGGAGGCGGAGGCGCGCGCGCGCGCGGAGGCTCGGCTCCGGC 286
 QY 30 ProSerAlaPheGlySerMetLys----- 37
 DB 287 CCAGCGCGCACCGCGCGGGAAGGCATCTGTGCGGGCCATGSGTGGGGGCGTCCGGGCGC 346
 QY 37 ----- 37
 DB 347 TCGAGCTCCGGGGTGGACCCGCGCGACCGCGCGGAGGCGAGGCGCGCGCGCGCA 406
 QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
 DB 407 GGCCTAGCTTCCCGCGCGCGGGGTGAAGCTGGGCGGTGCACGCGGAGGTTGACCACA 466
 QY 50 ValValAlaThrProGlnGlyProAspArgProGlnGluValSerThrAspThr 69
 DB 467 GTCTAGTCCACTCTAGGCCAAGGCCAGAGCGCTCCCAAGAGTGGCTTACACGGACATC 526
 QY 70 LysValIleGlyAsnGlySerPheGlyValValThrGlnAlaLysLysCysAspSerGly 89
 DB 527 AAGGTGATTGGCAATGGCTCATTTGGGGTGGTGTACAGGCGCGCGCTCGGAGACCGAGG 586

QY 90 GluLeuValAlaIleLysValLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109
 DB 587 GAACCTAGTCCCATCAGAGGTTCTCCAGGACCAAGAGGTTCCAGACCGAGAGCTGCAG 546
 QY 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheYrSerSer 129
 DB 647 ATCATGCGTAAGCTCGACCACTGCAATATTGTGAGGCTGAGATACTTTTCTACTCCAGT 706
 QY 130 GlyGluLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrVal 149
 DB 707 GCGCAGAGAAGAACGAGCGCTTTACCTAAATCTGGTGTGGAATATGTGCCGAGACAGTG 766
 QY 150 TyrArgValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLys 169
 DB 767 TACCGGTGGCGCGCCACTTCACCAAGGCCAAGTTGACCATCCCTTCTCTATGTCAGG 826
 QY 170 LeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHis 189
 DB 827 GTGTACATGTACCAGCTCTTCGCGAGCTTGGCTTACATCCACTCCAGGGGCGGTGTCTAC 886
 QY 190 ArgAspIleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCys 209
 DB 887 CGCGACATCAAGCCCGCAGACCTGCTGGTGGACCTGCACACTGCTGCTCAAGCTCTGC 946
 QY 210 AspPheGlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSer 229
 DB 947 GATTTGGCAGTGCACCAAGCTTGGTCCGAGGGGAGGCCCAATGTCTCTACATCTGTCT 1006
 QY 230 ArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAsp 249
 DB 1007 CCTACTACCGGCGCGCGAGAGCTCATCTTTGGAGCCACTGATTACACCTCATCATCAT 1066
 QY 250 ValTrpSerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGly 269
 DB 1067 GTTGTGCTGAGCTGGCTGTGACTGGCAGAGCTCTCTTGGCCAGCCCATCTTCCCTGGG 1126
 QY 270 AspSerGlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGlu 289
 DB 1127 GACAGTGGGCTGGACCACTGGTGGAGATCATCAAGGTGCTGGGAACCAACCAACCCGGAA 1186
 QY 290 GlnIleArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHis 309
 DB 1187 CAATTCGAGAGATGAACCCCACTACGAGAGTTCAAGTTCCCTCAGATTAAAGCTCAC 1246
 QY 310 ProTrpThrLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArg 329
 DB 1247 CCTGGCAAGAGTGTTCAAATCTCGNACCGCGCGAGGCCCATCGCGCTCTGCTCTAGC 1306
 QY 330 LeuLeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
 DB 1307 CTGCTGGAGTACACCCATCTCAAGGCTCTCCCACTAGAGGCTGTGGCAGACGCTTC 1366
 QY 350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369
 DB 1367 TTTGATCAACTGGCATGTCTCGGAACAGAGCTGCTTAAACACCGCCCACTTCCCTCTCTC 1426
 QY 370 PheAsnPheThrThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuLeuPro 389
 DB 1427 TTCAACTTCAGTGTGGTGAATCTTCATCCCAACCGTCTCTCAACGCCATTTTATTCCT 1486
 QY 390 ProHisAlaArg 393


```

Db      1487 CCTCACTTGAGG 1498
||||| |||
RESULT 5
CR615336
LOCUS   2119 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DC012VP11 of Neuroblastoma Cot
25-normalized of Homo sapiens (human).
ACCESSION CR615336
VERSION   CR615336.1 GI:50496143
KEYWORDS  HTC; CNSLT_cDNA.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Homnidae; Homo.
REFERENCE 1 (bases 1 to 2119)
AUTHORS   Li W.B., Gruber C., Jessee J. and Polayes D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 2119)
REFERENCE 2 (bases 1 to 2119)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES
source
1..2119
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DC012VP11"
/tissue_type="Neuroblastoma Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Alignment Scores:
Pred. No.: 6.48e-166 Length: 2119
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: 6 Gaps: 4
US-10-733-816-2 (1-394) x CR615336 (1-2119)
Qy      5 ProMetSerGlyArgProGlyThrSerPheAlaGluSer 23
||||| |||
Db      108 CCTTCGGGAGCGCGCTCGGGGCTCGGCGAGCGCGGACTAGCTCGTTCCGCGAG--- 164
||||| |||
Qy      24 CysIysPro-----ValGlnGln 29
|||||
Db      165 -----CCCGCGCGGAGCGGAGGAGCGCGCGCGCGCGCGCGCTCCGGC 218

```

/tissue type="Hela cells Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:

Pred. No.: 6,51e-166 Length: 2124
Score: 1609.00 Matches: 319
Percent Similarity: 77.3% Conservative: 24
Best Local Similarity: 71.8% Mismatches: 43
Query Match: 77.3% Indels: 58
DB: 6 Gaps: 4

US-10-733-816-2 (1-394) x CR593340 (1-2124)

QY 5 ProMetGluGlyCly---GlyMetSerGlyArgProArgThrThrSerPheAlaGluSer 23
Db 118 CCTTCGGGAGGCGCCCTGGGGGCTCGGGAGCGGAGCTAGCTCTTCGGGAG--- 174
QY 24 CyslyAspPro-----ValGlnGln 29
Db 175 -----CCCGCGCGGAGGCGGAGGCGGGCGGCGGAGGCTCGGGCTCCGGC 228
QY 30 ProSerAlaPheGlySerMetLys----- 37
Db 229 CCAGCGGCGACCGCGCGGCGGAAAGGCATCTGTGGGGCCATGTGGTGGGGCGTGGGGGCC 288
QY 37 ----- 37
Db 289 TCGAGCTCCGGGGTGGTGGACCGCGCGGCGGAGGCGGAGGCGGCGGCGCGCGCA 345
QY 38 -----ValSerArgAspLysAspGlySerLysValThrThr 49
Db 349 GGCCTAGCTTCCCGCGCGCGGGTGAAGCTGGGCGGTGACAGCGGGAAGGTGACCA 408
QY 50 ValValAlaThrProGlyGlnGlyProAspArgProGlnGluValSerThrAspThr 69
Db 409 GTCTAGGCACTCTAGGCGCAAGCGCGCGGAGCGCTCCCAAGAGTGGCTTACACGACATC 468
QY 70 LysValIleGlyAsnGlySerPheGlyValValTyroGlnAlaLysLeuCyAspSerGly 89
Db 469 AAGTGATTGGCAATGGCTCATTTGGGGTCTGTACCGAGCGCGCTGGCAGAGACCG 528
QY 90 GluLeuValAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGln 109
Db 529 GAACCTAGTCGCCATCAAGAGAGTTCTCCAGGACAAAGAGTTCAAGAACCGAGAGTGCAG 588
QY 110 IleMetArgLysLeuAspHisCysAsnIleValArgLeuArgTyroPhePheTyroSer 129
Db 589 ATCATGCGTAAGCTGGACCACTGCAATATTTGGAGGCTGAGACTTTTCTACTCCAGT 648
QY 130 GlyGluLysLysAspGluValTyroLeuAsnLeuValLeuAspTyroValProGluThrVal 149
Db 649 GCGGAGAGAAAGACGAGCTTTACCTAAATCTGGTCTGGANATGTCCCGGAGACAGTG 708
QY 150 TyroArgValAlaAlaArgHisTyroSerArgAlaLysGlnThrLeuProValIleTyroVal 169
Db 709 TACCGGGTGGCGCGCACTTCCAAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAG 768
QY 170 LeuTyroMetTyroGlnLeuPheArgSerLeuAlaTyroIleHisSerPheGlyIleCysHis 189
Db 769 GTGTACATGTACCAGCTCTTCCGCGAGCTTGGCGCTACATCATCCATCCCGAGGGCGTGTCTCAC 828

QY 290 GlnIleArgGluMetAsnProAsnTyroThrGluPheLysPheProGlnIleLysAlaHis 309
Db 1119 CAATCCGAGAGATGACCCCACTACAGGAGTTCAAGTTCCCTCAGATTAAAGCTCAC 1178
QY 310 ProTrpThrLysValPheArgProArgThrProProGluAlaIleAlaLeuCySerArg 329
Db 1179 CCCTGGCAAAAGTGTTCNAATCTCGAACCGCGCAGAGCCATCGCGCTCTCTCTAGC 1238
QY 330 LeuLeuGluTyroThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhe 349
Db 1239 CTGCTGGAGTACACCCCACTCCCAAGGCTCTCCCACTAGAGGCGCTGTGGCGACAGCTTC 1298
QY 350 PheAspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeu 369
Db 1299 TTTGATGACTGGATGCTGGGAACCCAGCTGCTTAACACCGCCACTTCCCTCTC 1358
QY 370 PheAsnPheThrGlnGluLeuSerSerAsnProProLeuAlaThrIleLeuIlePro 389
Db 1359 TTCAACTTCAGCTGGTGGTGAACCTCTCCATCCACCGCTCTCTCAACGCCATTCTTATCCCT 1418
QY 390 ProHisAlaArg 393
Db 1419 CCTCACTTGAGG 1430

RESULT 6

CR593340

LOCUS

2124 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DK005YF06 of Hela cells Cot 25-normalized
of Homo sapiens (human).

ACCESSION

CR593340.1 GI:50474147

VERSION

HTC; CINSUT_CDNA.

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 2124)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2124)

REFERENCE

AUTHORS

TITLE

JOURNAL

Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by life technologies, a
division of invitrogen.

FEATURES

source

1. .2124
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK005YF06"

[illegible]

QY 83 AlalysLeuCyaspSerGlyGluLeuValAlalileLysValLeuGlnAspLysArg 102
 DB 1873 GCACGGCTGGCAGACGAGCACTAGTCCCATCAAGAGGTTCTCCAGGCAAGAGG 1932

QY 103 PhelysAsnArgLysGlnLeuMetArgLysLeuAspHisCysAsnileValArgLeu 122
 DB 1933 TTCAAGAACCGAGAGCTGCAGATCATGCTGAAGCTGGACCACTGCATATATTGTGAGGCTG 1992

QY 123 ArgTyrPhePheTyrSerGlyGluLysLysAspGluValTyrLeuAsnLeuValLeu 142
 DB 1993 AGATACTTTTCTACTCCAGTGGCGAGAGAAACAGAGCTTTACCTAAATCTGTGGTGTG 2052

QY 143 AspTyrValProGluThrValTyrArgValAlaAlaArgHisTyrSerArgAlaLysGlnThr 162
 DB 2053 GAATATGTGCGCGACAGTGTACCGGGTGGCGCCGACCTTCAACAGGCCAAGTTGACC 2112

QY 163 LeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyrIle 182
 DB 2113 ATCCCTATCTCTATGTCAAGGTGTACATGTACAGCTCTTCGCGAGCTTGGCTACATC 2172

QY 183 HisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuAspProAsp 202
 DB 2173 CACTCCAGGGCGGTGTCCACGCGACATCAAGCCCGAGAACCTCTGGTGGACCCCTGAC 2232

QY 203 ThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArgGlyGluPro 222
 DB 2233 ACTGTCTCTCAAGCTCTGCGATTTTGGCAGTGCAGAGCAGTGTGTCGAGGGAGGCC 2292

QY 223 AsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAlaThr 242
 DB 2293 AATGTCTCTTACATCTGTCTCGCTACTACCGGGCCCGAGAGCTCATCTTTGAGGCACT 2352

QY 243 AspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeuLeu 262
 DB 2353 GATTACACCTCATCATCATGTTTGTGTCAAGTGTGTGTACTGGCAGAGCTCTCTGTG 2412

QY 263 GlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIleIleLysVal 282
 DB 2413 GGCCAGGCCCATCTTCCCTGGGACAGTGGGGTGGACCAAGCTGTGTGAGATCATCAAGGTG 2472

QY 283 LeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPheLys 302
 DB 2473 CTGGGAACACCAACCCGGGAACAAATCCGAGAGATGAACCCCACTACCGAGTTCAG 2532

QY 303 PheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThrProGlu 322
 DB 2533 TTCCCTCAGATTAAAGCTCACCCCTGGACAAAGGTGTTCMAATCTCGAACCCGCCCAAG 2592

QY 323 AlalileAlaLeuCySerArgLeuLeuGluTyrThrProThrAlaArgLeuThrProLeu 342
 DB 2593 GCCATCGGGCTGTCTGTAGCTGTGGAGTACACCCCATCTCTCAAGGCTCTCCCACTA 2652

QY 343 GluAlaCysAlaHisSerPheAspGluLeuArgAspProAsnValLysHisProAsn 362
 DB 2653 GAGGCTGTGCGCACAGCTCTTTTGTATGAATCGCATGTCTGGGAACCCAGCTGCCTAAC 2712

QY 363 GlyArgAspThrProAlaLeuPheAsnPheThrThrGlnLeuSerSerAsnProPro 382
 DB 2713 AACCGCCCACTTCTCCCTCTCTTCAACTTCAAGTGTGTGTAAGTCTCCATCCCAACCGTCT 2772

QY 383 LeuAlaThrIleLeuIleProHisAlaArg 393
 DB 2773 CTCACCCCATCTCATCCCTCTCTACTTGAGG 2805

RESULT 9
 W18183
 LOCUS IMAGE:20087 Soares infant brain INIB Homo sapiens linear EST 01-MAY-1995
 DEFINITION IMAGE:20087, mRNA sequence.
 ACCESSION W18183.1 GI:1293857
 VERSION W18183.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1094)
 AUTHORS Lieuallen,K., Prange,C., Carrano,A. and Lennon,G.
 TITLE Sequencing of Chromosome 19 cDNA Clones
 JOURNAL Unpublished (1996)
 COMMENT Contact: Greg G. Lennon
 Human Genome Center, L-452
 Lawrence Livermore National Laboratory
 Livermore CA 94550
 Tel: 510 422 8361
 Fax: 510 422 2282
 Email: info@image.llnl.gov
 This fully sequenced clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Sequence is sense strand compiled from multiple reads covering both strands.
 Insert Length: 1094 Std Error: 0.00
 Seq primer: multiple.
 FEATURES
 Location/Qualifiers
 1..1094
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:G00-393-882"
 /db_xref="taxon:9606"
 /clone="IMAGE:20087"
 /sex="female"
 /dev_stage="73 days post natal"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares infant brain INIB"
 /note="Organ: whole brain; Vector: Lafmid BA; Site:1: Not I; Site:2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5': AACTGGAGAATTCCGGCCGAGGAATTTTTTTTTTTT 3'];
 double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN
 Alignment Scores:
 Pred. No.: 1.76e-160 Length: 1094
 Score: 1556.00 Matches: 295
 Percent Similarity: 90.7% Conservative: 25
 Best Local Similarity: 83.6% Mismatches: 33

Qy	311	TropThyLysValPheArgProArgThrProGluAlaIleAlaLeuCysSerArgLeu	330
Db	866	TGGACAAAGGTTTCAAAATCTCGAACCGCCGACAGCCATCGGGCTGTGCTTACGCTG	925
Qy	331	LeuGluTyrThrProThrAlaArgLeuThrProLeuGluAlaCysAlaHisSerPhePhe	350
Db	936	CTGGAGTACACCCATCTCTCAAGGCTCTCCCCACTAGAGGCTGTGCGCAGACTTCTT	985
Qy	351	AspGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPhe	370
Db	986	GATGAATCGCATGTCTGGGAACCCAGCTGCGCTTACACACGCCCACTTCCCTCTCTTC	1045
Qy	371	AsnPheThrThrGlnGluLeuSerSerAsnProProLeu	383
Db	1046	AACCTCAGTGTGTGTAAGTCTCTCCACCGTCTCTA	1084
RESULT 10			
LOCUS	CX795595	841 bp mRNA linear EST 31-JAN-2005	
DEFINITION	JGI_CAAJ11693.fwd NIH_XGC_tropBrn2 Xenopus tropicalis cDNA clone		
ACCESSION	IMAGE:7641717 5', mRNA sequence.		
VERSION	CX795595		
KEYWORDS	CX795595.1 GI:58350224		
SOURCE	EST.		
ORGANISM	Xenopus tropicalis (western clawed frog)		
REFERENCE	Xenopus tropicalis		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.		
TITLE	1 (bases 1 to 841)		
JOURNAL	Richardson,P., Lucas,S., Rokhsar,D., Dettter,J.C., Ng,D.C., Brokstein,P. and Lindquist,E.A.		
COMMENT	DOE Joint Genome Institute Xenopus tropicalis EST project Unpublished (2004) Other_ESTs: JGI_CAAJ11693.rev Contact: Lindquist,E.A., Richardson,P. DOE Joint Genome Institute 2800 Mitchell Drive, Walnut Creek, CA 94598, USA Tel: 925 296 5600 Fax: 925 296 5710 Email: cdna@jgi-psf.org Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley) http://tropicalis.berkeley.edu/home/ cDNA Library Preparation: DOE Joint Genome Institute: http://www.jgi.doe.gov DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov Clone Imagebank: I.M.A.G.E. Consortium/LLNL: http://image.llnl.gov Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert. Plate: CNAJ 0121 row: j column: 19 High quality sequence stop: 794. Location/Qualifiers 1. .841 /organism="Xenopus tropicalis" /mol_type="mRNA" /db_xref="taxon:8364" /clone="IMAGE:7641717"		
FEATURES			
SOURCE			

```

/tissue_type="Brain"
/dev_stage="Adult"
/lab_host="ElectroMAX DH108"
/clone_lib="NIH_XCG_tropBrn2"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
This library was made from dt primed cDNA and cloned into
Invitrogen pCMVSPORT6 vector. The work was done at DOE
Joint Genome Institute. Poly A RNA were primed with 5'
GACTAGTCTAGATCCGAG CGGCCGCTTTT TTTT 3'. cDNA
were ligated to SalI adapter (5' TCGACCCACGCGCCG and
5'CGACCGCGGG), digested with NotI, size fractionated in
1.1% agarose gel electrophoresis and ligated into NotI and
SalI digested pCMVSPORT6 vector."

```

ORIGIN

Alignment Scores:

```

Pred. No.: 1.68e-148 Length: 841
Score: 1446.00 Matches: 274
Percent Similarity: 98.9% Conservative: 3
Best Local Similarity: 97.9% Mismatches: 3
Query Match: 69.5% Indels: 0
DB: 9 Gaps: 0

```

US-10-733-816-2 (1-394) x CX795595 (1-841)

```

QY 42 LysaspGlySerIyValThrValValAlaThrProGlyGlnGlyProAspArgPro 61
DB 2 MAAGATGCCAGCAAGTACACAGTAGTAGCGACCCCGCGGCGCGCGCGCGAG 61
QY 62 GlnGluValSerIyThrAspThrIyValIleGlyAsnGlySerPheGlyValValTyr 81
DB 62 CAAGAAGTCAGTCACCGCACCAAGGTTATTGGCAAGCGGTCTTTGGGGTGTGTAC 121
QY 82 GlnAlaIySerIyCysAspSerGlyGluLeuValAlaIleIyLysValLeuGlnAspIy 101
DB 122 CAGGCCAAACTGTGCGACACCGGGAGCTGTGGCTATCAGAAGTGTCTACAGCAAG 181
QY 102 ArgPheIyAsnArgLeuGlnIleMetArgIyLysLeuAspHisCysAsnIleValArg 121
DB 182 AGATTTAAGAACCGAGAACTGCAGATCATGAGAAAACCTGCATCTGCACATTTGGCGT 241
QY 122 LeuArgTyrPhePheTyrSerSerGlyGluIyLysAspGluValTyrLeuAsnLeuVal 141
DB 242 CTGGCGTACTTCTTCTCTCCAGCGGGAGAGAGAGCAAGTGTACCTCAACTTGGTG 301
QY 142 LeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAlaIyGln 161
DB 302 CTGGACTACGTTCCCGAACTGTGTACAGAGTGGCCAGACATTACAGCCGGGCTAAGCAG 361
QY 162 ThrLeuProValIleTyrValIyLysLeuTyrMetTyrGlnLeuPheArgSerLeuAlaTyr 181
DB 362 GCGTCCCGCATGATCTATGTCAGTTGTACATGTACAGCTGTTCGGAGTTTAGCCTAC 421
QY 182 IleHisSerPheGlyIleCysHisArgAspIleIySerProGlnAsnLeuLeuAspPro 201
DB 422 ATCCATTCTTTGGGATCTGCCCGGGATATCAACACAGAACCTTCTGCTGGACCCA 481
QY 202 AspThrAlaValLeuIySerIyCysAspPheGlySerAlaIyGlnLeuValArgGlyGlu 221
DB 482 GAAACTGCTGTACTCAAGCTGTGTGCTTTTGGCAGTGTCCCAAGCAGCTGTGACCGGAG 541

```

```

QY 222 ProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePheGlyAla 241
DB 542 CCCAACGTGTCTACATCTCTCCGGTACTACAGGCCCCCAGAGTTGATCTTTGGAGCC 601
QY 242 ThrAspTyrThrSerSerIleAspValTrpSerAlaGlyCysValLeuAlaGluLeuLeu 261
DB 602 ACCGATTACACTTCCAGCTATTACGCTGTGGTCAGCAGGCTGGGTATTGGCGGAGCTGCTG 661
QY 262 LeuGlyGlnPheProGlyAspSerGlyValAspGluLeuValGluIleIleLys 281
DB 662 CTGGGTGAGCCCATCTTCTTGGGGACAGCGCGTGGATCAGCTGGTTGAGATAATCAAG 721
QY 282 ValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThrGluPhe 301
DB 722 GTTCTGGGTACCCCGCTCTGGAGCAGATCCGAGAAATGAAACCACTACACTGATTC 781
QY 302 LysPheProGlnIleIyLysAlaHisProTrpThrLysValPheArgProArgThrProPro 321
DB 782 AAGTTCCACAGATAAGGCGCATCTTGGCAAAAGTGTTCGGGGCGCGCACCCCTCC 841
RESULT 11
DN530922/c 818 bp mRNA linear EST 11-MAR-2005
LOCUS 1358786 MARC 7BOV Bos taurus cDNA 3', mRNA sequence.
DEFINITION DN530922
ACCESSION DN530922
VERSION DN530922.1 GI:60976699
KEYWORDS EST.
SOURCE Bos taurus (cattle)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 818)
AUTHORS Smith,T.P.L., Roberts,A.J., Echtenkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keefe,J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: RLK8053 row: M column: 14
Seq primer: TAGAGGCACAGTCGAGG.
FEATURES
source
1..818
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
/clone_lib="MARC 7BOV"
/notes="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including ovary, hindbrain, uterus, and day-30 whole
embryos."
ORIGIN

```

Alignment Scores:
 Pred. No.: 4,286-145 Length: 818
 Score: 1415.00 Matches: 271
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 68.0% Indels: 0
 DB: 9 Gaps: 0

US-10-733-816-2 (1-394) x DNS30922 (1-818)

QY 35 SerMetLysValSerArgAspLysAspGlySerLysValThrThrValValAlaThrPro 54
 |||||
 DB 816 AGCATGAAGTTAGCAGACAGCAAGATGCGCAGCAAGTGCACAGTGGTGGCACTCCT 757
 |||||

QY 55 GlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLysValIleGlyAsn 74
 |||||
 DB 756 GGGCAGGGTCCAGACAGCCACAGCAAGTCAAGTATACAGACACTAAAGTGAATGCGAAT 697
 |||||

QY 75 GlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaIle 94
 |||||
 DB 696 GGGTCATTTGGTGTCTGTATCAAGCCAACTTTGTGATTCAGGAGAACTGGTGCCATC 637
 |||||

QY 95 LysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeu 114
 |||||
 DB 636 AAGAAAGTATTCAGACAGACAGATTTAAGACCGAGAGCTCCAGATCATGAGAAAGCTA 577
 |||||

QY 115 AspHisCysAsnIleValArgLeuArgTyrPheTyrSerSerGlyGluLysLysAsp 134
 |||||
 DB 576 GATCACTGTAACATAGTCCGATTGCGTTATTTCTTACTCAAGTGGTGAAGAAAGAT 517
 |||||

QY 135 GluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArgValAlaArg 154
 |||||
 DB 516 GAGGTCTATCTTAATCTGCTGGACTACGTTCCGAAACAGCTACAGAGTCGCCAGA 457
 |||||

QY 155 HisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyrMetTyrGln 174
 |||||
 DB 456 CACTATAGTCGAGCCAAACAGAGCGCTCCCTGTGATCTATGTCAGTTGTATATGTATCAG 397
 |||||

QY 175 LeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArgAspIleLysPro 194
 |||||
 DB 396 CTGTTCCGAAGTTTACCTATATCCATTCCTTTGGAACTCTGCCATCGGGATATTAAACA 337
 |||||

QY 195 GlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPheGlySerAla 214
 |||||
 DB 336 CAGAACTCTTGTGGATCCTGATACAGCTGTCTTGAACCTCTGTGACTTTGGAAGTSCA 277
 |||||

QY 215 LysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyrTyrArgAla 234
 |||||
 DB 276 AAGCAGCTGCTCGTGGAGAACCCCAATGTTTCGTATATCTGTCTCGTACTATAGGCA 217
 |||||

QY 235 ProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspValTyrSerAlaGly 254
 |||||
 DB 216 CCAGAGTTGATCTTTGGAGCCACTGATATATACCTCTAGTATAGATGTATGGTCTGCAGGC 157
 |||||

QY 255 CysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAspSerGlyValAsp 274
 |||||
 DB 156 TGTGTGTGGCTGACCTGCTAGCAGACCAATATTTCCAGAGACAGCTGTGTGGAT 97
 |||||

QY 275 GlnLeuValGluIleLysValLeuGlyThrProThrArgGluGlnIleArgGluMet 294
 |||||

96 CAGTGTGGTGAATAATCAAGGTCTGGGACACCAACAGGGAGCAAAATTCGAGAAATG 37

295 AsnProAsnTyrThrGluPheLysPheProGln 305
 |||||

36 AACCCAAACTACACGGAATTCAAATTCCTCTCA 4

RESULT 12
 CO579074

LOCUS CO579074 993 bp mRNA linear EST 20-JUL-2004
 DEFINITION ILLUMINEN_MQ_50668 Katze_MMIL Macaca mulatta cDNA clone
 ILIUM:16936 5' similar to Bases 5 to 992 highly similar to human
 GSK3A (Hs.435970), mRNA sequence.

ACCESSION CO579074
 VERSION CO579074.1 GI:50409944
 KEYWORDS EST.

SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Cercopithecoidea; Cercopithecinae; Macaca.

REFERENCE 1 (bases 1 to 993)
 MAGNESS,C.L., FELLIN,P.C., THOMAS,M.J., KORTH,M.J., AGY,M.B.,
 PROLL,S.C., FITZGIBBON,M., SCHERER,C.A., MINER,D.G., KATZE,M.G. and
 IADONATO,S.P.
 Analysis of the Macaca mulatta transcriptome and the sequence
 divergence between Macaca and human
 Genome Biol. 6 (7), R60 (2005)
 15998449

JOURNAL PUBMED
 COMMENT Contact: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.07.16. 702 Q20 bases. Library Preparation: Prcf.
 Michael Katze Lab at University of Washington DNA Sequencing:
 Illumigen Biosciences Inc. For further information, see
 http://www.macaque.org

PCR Primers
 FORWARD: CCTCACTAAAGGGAACAAA
 BACKWARD: CACTATAGGCGAATTGGTA
 Insert Length: 993 Std Error: 0.00
 Plate: CL000422 row: E column: 09
 Seq primer: CCTCACTAAAGGGAACAAA
 POLYA-No.

FEATURES
 Location/Qualifiers
 1..993
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIUM:16936"
 /sex="male"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katze_MMIL"
 /notes="Organ: ileum; Vector: pDONR 222; Site 1: BarG I;
 Site 2: BarG I; Created from Clonewiner cDNA Library
 Construction kit (catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.: 1-78e-144 Length: 993
 Score: 1410.50 Matches: 274
 Percent Similarity: 88.6% Conservative: 22
 Best Local Similarity: 82.0% Mismatches: 25
 Query Match: 67.8% Indels: 13
 DB: 8 Gaps: 2

US-10-733-816-2 (1-394) x C0579074 (1-993)

QY 52 AlaThrProGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLysVal 71
 DB 5 GCCACTCTAGGCCAAGGTCACAGAGCGCTCCCAAGAGGTGCTTACACAGACATCAAGTG 64
 QY 72 IleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGluLeu 91
 DB 65 ATTGGCAATGGCTATTGGGGTGGTGTACCGAGCGCTGGCAGACGACCGGAACTG 124
 QY 92 VallAlaIleLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMet 111
 DB 125 GTCCGCATCAAGAGGTTCTCCAGGACAAGAGGTTCAAGAACCGAGAGCTGCAGATCATG 184
 QY 112 ArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGlyGlu 131
 DB 185 CGTAAGCTGCACCATCGCATATTGTGAGCTGAGATACTTTTCTACTCCAGTGGGAG 244
 QY 132 LysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArg 151
 DB 245 AAGAAGATGAGCTTTACCTAATCTGGTGTGGAATATGTGCCCGAGACAGTGTACCGG 304
 QY 152 VallAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyr 171
 DB 305 GTGGCCGCCACTTACCAGAGCCAAAGTTGACCATCTCTATCTATGCAAGGTGATC 364
 QY 172 MetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArgAsp 191
 DB 365 ATGTACCAGCTCTTCGAGCTTGGCTACATCCACTCCAGCGGCTGTGTACCTGAC 424
 QY 192 IleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPhe 211
 DB 425 ATCAAGCCCCAGAACCTCTGCTGGACCTTGACACTGCTCTCTACATCTGTCTCCTAC 484
 QY 212 GlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyr 231
 DB 485 GCGAGTGGGAAGCAGTGTGCTCCGAGGGAGCCCAATGTCTCTACATCTGTCTCCTAC 544
 QY 232 TyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerIleAspValTyr 251
 DB 545 TACCGGGCCCAAGCTCATCTTTGGAGCCACTGATTACACCTCATCTCATCGATGTTGG 604
 QY 252 SerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAspSer 271
 DB 605 TCAGCTGGCTGCTACTGGCGAGCTCTCTCTGGCCAGCCCATTTCTCTGGGAGACGT 664
 QY 272 GlyValAspGlnLeuValIleLysValLeuGlyThrProThrArgGluGlnIle 291
 DB 665 GGGGTGACCAAGCTGTGGAGATCATCAAGGTGCTGGACACCAACCCCGGACCAATC 724
 QY 292 ArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyr 311
 DB 725 CGAGAGATGAACCCCAACTACACGAGTTTCATGTTCTCCATTAAGATTAAGCTCACCCCTGG 784

QY 312 ThrLysValPheArgProArgThrProGluAlaIleAlaLeuLysSerArgLeuLeu 321
 DB 785 ACRAAGGTGTTCAATCTCGAACCCCGCAGAGCATCCGCTGTGCTTACCTACCTGCTG 844
 QY 332 GluTyrThrProThrAlaArgLeu-ThrProLeuGluAlaCysAlaHisSerPhe-PheA 351
 DB 845 GAGTACCCCGCCGCTCAAGGCTCCCGCCCTTAAAGAGCTGCGCACACAGCTTCTCTTG 904
 QY 351 spGluLeuArgAspProAsnValLysHisProAsnGlyArgAspThrProAlaLeuPheA 371
 DB 905 AAGAAGCTGCGAAGCGCGGG-----AACCCAGCTCCCTTAAAAAACCCCCCACTTC- 937
 QY 371 snPheThrThrGlnGluLeuSerSerAsnProProLeu 383
 DB 958 -----CCCCCCCCCTT 969
 RESULT 13
 DT309300
 LOCUS DT309300
 DEFINITION JGI_CAA1138.fwd CAA1138 promelas testis 7-8 month adults, males and females pooled (L) Pimephales promelas cDNA clone CAA1138 5', mRNA sequence.
 ACCESSION DT309300
 VERSION DT309300.1 GI:73649963
 KEYWORDS EST.
 SOURCE Pimephales promelas
 ORGANISM Pimephales promelas
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Pimephales.
 REFERENCE 1 (bases 1 to 869)
 AUTHORS Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C., Brokstein, P., and Lindquist, E.A.
 TITLE DOE Joint Genome Institute Pimephales promelas EST project Unpublished (2005)
 JOURNAL Other_ESTs: JGI_CAA1138.rev
 COMMENT Contact: Lindquist, E.A., Richardson, P.
 DOE Joint Genome Institute
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
 Tel: 925 296 5600
 Fax: 925 296 5710
 Email: cdna@jgi-psf.org
 cDNA Library Preparation: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the orientation of the insert.
 Plate: CAA1138 row: d column: 22
 High quality sequence stop: 788.
 Location/Qualifiers
 1. 869
 /organism="Pimephales promelas"
 /mol_type="mRNA"
 /db_xref="taxon:90988"
 /clone="CAA1138"
 /tissue_type="testis"
 /clone_lib="CAA1138 Pimephales promelas testis 7-8 month adults, males and females pooled (L)"

/note="Vector: pCMVSPORT6; The library was made from dT primed cDNA and cloned into invitrogen vector pCMVSPORT6. Poly A RNA were primed with an oligo dT primer (5'-GACTAGTCTTAGATCGGAGCGCGCCCTTTTITTTT -3') ligated to a SalI adapter (5'-TCGACCAACGCGCCG and 5'-CGACCGCTGGG) and digested with NotI. cDNA was size selected using 1.1% agarose gel electrophoresis (L -0.5-1.2k, M -1.2-2.5k, H ->2.5k) then ligated into NotI and SalI digested pCMVSPORT6 vector. The work was done at DOE Joint Genome Institute."

ORIGIN

Alignment Scores:
 Pred. No.: 9,88e-144 Length: 869
 Score: 1403.00 Matches: 258
 Percent Similarity: 96.5% Conservative: 20
 Best Local Similarity: 89.6% Mismatches: 10
 Query Match: 67.4% Indels: 0
 DB: 10 Gaps: 0

US-10-733-816-2 (1-394) x DT039300 (1-869)

Qy 80 ValTyrGlnAlaLysLeuCysAspSerGlyGluLeuValAlaLysValLeuGln 99
 Db 3 GTGTACACGGCTCGACTCATCTGCACGAGGAGATGGCCATAAGAGGCTTCAG 62
 Qy 100 AspLysArgPheLysAsnArgGluLeuGlnLeuMetArgLysLeuAspHisCysAsnIle 119
 Db 63 GATAACGGTTTAAAGACCGTGGAGTATGAGGAGTGGACCACTGTATAT 122
 Qy 120 ValArgLeuArgTyrPhePheTyrSerSerGlyGluLysAspGluValTyrLeuAsn 139
 Db 123 GTACGGCTAGCTACTTCTCTACTCCAGTGAGAGAAAGATGAATGTATCAAT 182
 Qy 140 LeuValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAla 159
 Db 183 CTGGTGCTGGATTTGTTCCAGAACTGTGTACAGGCTGGCAGCCATTTCAACAGTCC 242
 Qy 160 LysGlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeu 179
 Db 243 AAGACCACCTCCCTCATCTATGTCAAAGTATATGTATCAGTTATTCGAGCTGTG 302
 Qy 180 AlaTyrIleHisSerPheGlyIleCysHisArgAspIleLysArgProGlnAsnLeuLeu 199
 Db 303 GCGTATATTCATTCGAGGCGTCCGATAGACATCAAGCCACAGATCTCCTGGTG 362
 Qy 200 AspProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArg 219
 Db 363 GACCCAGACACAGCTGTACTCAAACTGTGTACATTGGCAGTGCAAAACAGTTAGTTCT 422
 Qy 220 GlyGluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePhe 239
 Db 423 GGGGAGGCCAATGTGTACATACATCTGTCCGGTATTACCGGCTCTGAGCTTAATTC 482
 Qy 240 GlyAlaThrAspTyrThrSerIleAspValTyrSerAlaGlyCysValLeuAlaGlu 259
 Db 483 GGAGCCAGGATTCACATTCACATGTATCTGTGTCAGCGCTGTGTATAGCAGAG 542
 Qy 260 LeuLeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluTle 279
 Db 543 CTGCTTTTGGGACAGCCCATATTCCTCCGGGTGACAGTGGAGTGACCACTAGTGAGATC 602

Qy 280 IleLysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThr 293
 Db 603 ATCAAGGTTTTGGGAGCCCCACAGAGAACAGATCCGAGAGATGAACCCCACTACACA 662
 Qy 300 GluPheLysPheProGlnIleLysAlaHisProTyrThrLysValPheArgProArgThr 319
 Db 663 GAGTTTAAATTTCCACAGATCAAGCACACCTTGGACAAAGGTGTTTACCGGAGACC 722
 Qy 320 ProProGluAlaIleAlaLeuCysSerArgLeuLeuGluTyrThrProThrAlaArgLeu 339
 Db 723 CCTCTGAAGCCATCTCATTTCTCTCTGTGTGTACACGCGGTGACGCGGCTC 782
 Qy 340 ThrProLeuGluAlaCysAlaHisSerPhePheAspGluLeuArgAspProAsnValLys 359
 Db 783 TCGCCGCTGGAGGCTGTGCACATGCTTCTTTGATGAGCTGCGCAGCCGACGACCT 842
 Qy 360 HisProAsnGlyArgAspThrPro 367
 Db 843 CTGCTTAATGCGGAGAACTTCCC 866

RESULT 14

AK164048 2190 bp mRNA linear HTC 21-SEP-2005
 Mus musculus 7 days embryo whole body cDNA, RIKEN full-length
 enriched library, clone:C430034M07 product:glycogen synthase kinase
 3 beta, full insert sequence.
 AK164048
 AK164048.1 GI:74208723
 HTC; CAP trapper.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujikawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 11076861
 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

- Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Cavaant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, T., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Waehio, T., Sakai, K., Okido, T., Furuno, M., Anno, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyooka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
- RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium
- Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
11217851
- 5
- Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oatono, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Brad, D., Brusica, V., Chochocka, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maitais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yagunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
- FANTOM Consortium
- Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420 (6915), 563-573 (2002)
12466851
- 6
- Carninci, P., Kasukawa, T., Katayama, S., Gough, J., Frith, M.C., Maeda, N., Oyama, R., Ravasi, T., Lenhard, B., Wells, C., Kodzrus, R., Shimokawa, K., Bajic, V.B., Brenner, S.E., Batalov, S., Forrest, A.R., Zavolan, M., Davis, M.J., Wilming, L.G., Aidinis, V., Allen, J.E.,
- Ambsi-Impiombato, A., Apweiler, R., Aturaliya, R.N., Bailey, T.L., Bansal, M., Baxter, L., Beisel, K.W., Bersano, T., Bono, H., Chalk, A.M., Chiu, K.P., Choudhary, V., Christoffels, A., Clutterbuck, D.R., Crowe, M.L., Dalla, E., Dalrymple, B.P., de Bono, B., Della Gatta, G., Di Bernardo, D., Down, T., Engstrom, P., Fagiolini, M., Faulkner, G., Fletcher, C.F., Fukushima, T., Furuno, M., Futaki, S., Gariboldi, M., Georgi-Hemming, P., Gingeras, T.R., Gojobori, T., Green, R.E., Gustincich, S., Harbers, M., Hayashi, Y., Hensch, T.K., Hirokawa, N., Hill, D., Hummel, L., Iacono, M., Ikeo, K., Iwama, A., Ishikawa, T., Jake, M., Kanapin, A., Katoh, M., Kawasawa, Y., Keiso, J., Kitamura, H., Kitano, H., Kollas, G., Krishnan, S.P., Kruger, A., Kummerfeld, S.K., Kurochkin, I.V., Lareau, L.F., Lazarevic, D., Lipovich, L., Liu, J., Liuni, S., McWilliam, S., Madan, Babu, M., Madera, M., Marchionni, L., Matsuda, H., Matsuzawa, S., Miki, H., Mignone, F., Miyake, S., Morris, K., Mottagui-Tabar, S., Mulder, N., Nakano, N., Nakachi, H., Ng, P., Nilsson, R., Nishiguchi, S., Nishikawa, S., Nori, F., Ohara, O., Okazaki, Y., Orlando, V., Pang, K.C., Pavan, W.J., Pavese, G., Pesole, G., Petrovsky, N., Piazza, S., Reed, J., Reid, J.P., Ring, B.Z., Ringwald, M., Rost, B., Ruan, Y., Salzberg, S.L., Sandelin, A., Schneider, C., Schonbach, C., Sekiguchi, K., Semple, C.A., Seno, S., Sessa, L., Sheng, Y., Shibata, Y., Shimada, H., Shimada, K., Silva, D., Sinclair, B., Sperling, S., Stupka, E., Sugiyama, K., Sultana, R., Takenaka, Y., Taki, K., Tammoja, K., Tan, S.L., Tang, S., Taylor, M.S., Tegner, J., Teichmann, S.A., Ueda, H.R., van Nimwegen, E., Verardo, R., Wei, C.L., Yagi, K., Yamanishi, H., Zabarovsky, E., Zhu, S., Zimmer, A., Hide, W., Bult, C., Grimond, S.M., Teasdale, R.D., Liu, E.T., Kusic, V., Quackenbush, J., Wahlestedt, C., Mattick, J.S., Hume, D.A., Braich, C., Sasaki, D., Tomaru, Y., Fukuda, S., Kanamori, K., Katayama, M., Suzuki, M., Aoki, J., Arakawa, T., Iida, J., Imamura, K., Itoh, M., Kato, T., Kawaji, H., Kawagashira, N., Kawashima, T., Kojima, M., Kondo, S., Konno, H., Nakano, K., Ninomiya, N., Nishio, T., Okada, M., Plessey, C., Shibata, K., Shiraki, T., Suzuki, S., Tagami, M., Waki, K., Wachihi, A., Okamura-Oho, Y., Suzuki, H., Kawai, J. and Hayashizaki, Y.
- FANTOM Consortium
- The transcriptional landscape of the mammalian genome
Science 309 (5740), 1559-1563 (2005)
16141072
- 7
- Katayama, S., Tomaru, Y., Kasukawa, T., Waki, K., Nakanishi, M., Nakamura, M., Nishida, H., Yap, C.C., Suzuki, M., Kawai, J., Suzuki, H., Carninci, P., Hayashizaki, Y., Wells, C., Frith, M., Ravasi, T., Fang, K.C., Hallinan, J., Mattick, J., Hume, D.A., Lipovich, L., Batalov, S., Engstrom, P.G., Mizuno, Y., Faghihi, M.A., Sandelin, A., Chalk, A.M., Mottagui-Tabar, S., Liang, Z., Lenhard, B. and Wahlestedt, C.
- RIKEN Genome Exploration Research Group
- Antisense transcription in the mammalian transcriptome
Science 309 (5740), 1564-1566 (2005)
16141073
- 8 (bases 1 to 2190)
- Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hori, F., Iida, J., Imamura, K., Imotani, K., Itoh, M., Kanagawa, S., Kawai, J., Kojima, M., Konno, H., Murata, M., Nakamura, M., Ninomiya, N., Nishiyori, H., Nomura, K., Ohno, M., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shiraki, T., Tagami, M., Tagami, Y., Waki, K., Wachihi, A., Muramatsu, M. and Hayashizaki, Y.
- Direct Submission
- Submitted (14-APR-2004) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa, 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

COMMENT
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/

FEATURES
Location/Qualifiers

1. .2190

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CS7BL/6"

/db_xref="FANTOM DB:C430034M07"

/db_xref="taxon:10090"

/clone="C430034M07"

/tissue_type="whole body"

/clone_lib="RIKEN full-length enriched mouse cDNA library"

/dev_stage="7 days embryo"

1. .2190

/note="glycogen synthase kinase 3 beta (MGD|MG1:1861437

GB|BC006936, evidence: BLASTN, 100%, match=788)

putative"

misc_feature

ORIGIN

Alignment Scores:

Pred. No.: 2-22e-141 Length: 2190
Score: 1387.00 Matches: 263
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 66.7% Indels: 0
DB: 6 Gaps: 0

US-10-733-816-2 (1-394) x AK164048 (1-2190)

QY 52 AlaThrProGlyGlnGlyProAspArgProGlnGluValSerTyrThrAspThrLysVal 71
|||||
DB 1 GCAACTCTGCGCCAGGCTCTGACAGGCCACAGGAGTCAGTTATACAGACGAAAGTG 60
QY 72 IleGlyAsnGlySerPheGlyValValTyrGlnAlaLysLeuCysAspSerGlyGluLeu 91
|||||
DB 61 ATTGMAATGCATCTATTGGTGTGTATATCAAGCCAAACTTTGTGATTTCTGGAGAACTG 120
QY 92 ValAlaLysLysLysValLeuGlnAspLysArgPheLysAsnArgGluLeuGlnIleMet 111
|||||
DB 121 GTTGCCATCAAGAAAGTTCTACAGGACAGCGAATTAAGAACCGAGAGCTCCAGATCATG 180
QY 112 ArgLysLeuAspHisCysAsnIleValArgLeuArgTyrPhePheTyrSerSerGlyGlu 131
|||||
DB 181 AGAAGCTAGACCACTGTATACATAGTCCGACTGCGGTATTTCTTACTCGAGTGGTGAG 240
QY 132 LysLysAspGluValTyrLeuAsnLeuValLeuAspTyrValProGluThrValTyrArg 151
|||||
DB 241 AAGAAGATGAGGTCTACCTTAACCTGGTGGTACTATGTTCCGAGACAGAGTGTACAGA 300
QY 152 ValAlaArgHisTyrSerArgAlaLysGlnThrLeuProValIleTyrValLysLeuTyr 171
|||||
DB 301 GTCCGACACACTATAGTCGAGCCAGCAGACACTCCCTGTGATCTATGTCAGTTGTAT 360

QY 172 MetTyrGlnLeuPheArgSerLeuAlaTyrIleHisSerPheGlyIleCysHisArgAsp 191
|||||
DB 361 ATGATATCAGCTGTTCAGAGCTAGCTATATCCATTCCTTTGGATCTGCCATCGACAC 426
QY 192 IleLysProGlnAsnLeuLeuAspProAspThrAlaValLeuLysLeuCysAspPhe 212
|||||
DB 421 ATTAACACACAGAACCTCTCTGTTGGATCTCTGATACAGCTGATATTAATAAACTCTGTGACTT 489
QY 212 GlySerAlaLysGlnLeuValArgGlyGluProAsnValSerTyrIleCysSerArgTyr 231
|||||
DB 481 GGAAGTCAAGCAGCTGCTCCGAGGAGAGCCCAATGTTTCATATATCTGTTCTCGGTAC 540
QY 232 TyrArgAlaProGluLeuIlePheGlyAlaThrAspTyrThrSerSerIleAspValTyr 251
|||||
DB 541 TACGGCACCAGAGTTGATCTTTGGAGCCACTGATTCACGTCCTCATGATAGATGTGG 600
QY 252 SerAlaGlyCysValLeuAlaGluLeuLeuGlyGlnProIlePheProGlyAspSer 271
|||||
DB 601 TCTGCAGGCTGTGCTGTGGCTGAATTGTTGCTAGGACACCAATATTTCTCTGGGACAGT 660
QY 272 GlyValAspGlnLeuValGluIleLysValLeuGlyThrProThrArgGluGlnIle 291
|||||
DB 661 CGTGTGGATCAGTTGTGGTGAATAATAAAGGTCTTAGGAAACCAACCAAGGAGCAATT 720
QY 292 ArgGluMetAsnProAsnTyrThrGluPheLysPheProGlnIleLysAlaHisProTyr 311
|||||
DB 721 AGAGAAATGAACCCAAATTATACAGAAATTCAAATTCCTCAATCAAGGCACATCTCTGG 780
QY 312 ThrLysVal 314
|||||
DB 781 ACAAGGTG 789
RESULT 15
BO651422
LOCUS BO651422
DEFINITION AGENCOURT_8341134 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6268349
5', mRNA sequence.
ACCESSION BO651422
VERSION BO651422.1 GI:21775594
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 890)
AUTHORS NIH-MGC http://mgi.mgi.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@pba-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2440 row: c column: 06
High quality sequence stop: 717.

FEATURES

Location/Qualifiers

1. 890
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6268349"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_100"
 /note="Organ: liver; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 4 57e-141 Length: 890
 Score: 1379.00 Matches: 262
 Percent Similarity: 94.9% Conservative: 17
 Best Local Similarity: 89.1% Mismatches: 13
 Query Match: 66.3% Indels: 2
 DB: 3 Gaps: 0

US-10-733-816-2 (1-394) x BQ651422 (1-890)

QY 60 ArgProGlnGluValSerTyrThrAspThrLysValIleGlyAsnGlySerPheGlyVal 79
 DB 3 CCCTCCCAAGAGTGGCTTACACGACATCAAGTGATTGGCAATGGCTCATTTGGGTC 62
 QY 80 ValTyrGlnAlaLysLeuCysAspSerGlyGluValAlaLysLysValLeuGln 99
 DB 63 GTGTACACGACGCGTGGCAGACACCGGAACTAGTCCCATCAGAAGGTTCTCCAG 122
 QY 100 AspLysArgPheLysAsnArgGluLeuGlnIleMetArgLysLeuAspHisCysAsnIle 119
 DB 123 GACAGAGGTTCAAGAACCGAGAGCTGCAGATCATGGTAAGCTGGACCACTGCAATATT 182
 QY 120 ValArgLeuArgTyrPhePheTyrSerSerGlyGluLysLysAspGluValTyrLeuAsn 139
 DB 183 GTGAGGCTGAGATACTTTTCTACTCCAGTGGCGAGAAGAACGACGACTTTACCTAAAT 242
 QY 140 LeuValLeuAspTyrValProGluThrValTyrArgValAlaArgHisTyrSerArgAla 159
 DB 243 CTGGTGCTGGAATATGTCCCGAGACAGTGTACCGGGTGGCCCGCCACTTCACCAAGGCC 302
 QY 160 LysGlnThrLeuProValIleTyrValLysLeuTyrMetTyrGlnLeuPheArgSerLeu 179
 DB 303 AAGTTGACCATCTCTATCTATGTCAAGGTGTACATGTACCATCTCTCCGACGTG 362
 QY 180 AlaTyrIleHisSerPheGlyIleCysHisArgAspIleLysProGlnAsnLeuLeuLeu 199
 DB 363 GCCTACATCCACTCCCGGGGGTGTGTACACCGGACATCAGCCCCAGAACCTGCTGTG 422
 QY 200 AspProAspThrAlaValLeuLysLeuCysAspPheGlySerAlaLysGlnLeuValArg 219
 DB 423 GACCCTGACACTGCTGCTCTCAAGCTCTGCCATTTGGCAGTGCAAGCAGTTGGTCCGA 482

QY 220 GlyGluProAsnValSerTyrIleCysSerArgTyrTyrArgAlaProGluLeuIlePhe 239
 DB 483 GGGGAGCCCAATGTCTCTACATCTGTCTGCTACTACCGGGCCCCAGAGCTCATCTTT 542
 QY 240 GlyAlaThrAspTyrThrSerSerIleAspValTyrSerAlaGlyCysValLeuAlaGlu 259
 DB 543 GGAGCCACTGATTACACCTCATCCATCGATGTTGGTCAGCTGGCTGTGTACTGGCAGAG 602
 QY 260 LeuLeuLeuGlyGlnProIlePheProGlyAspSerGlyValAspGlnLeuValGluIle 279
 DB 603 CTCTCTTGGGCCAGCCCATCTTCCCTGGGGACAGTGGGTGGACACAGCTGGTGGAGATC 562
 QY 280 IleLysValLeuGlyThrProThrArgGluGlnIleArgGluMetAsnProAsnTyrThr 299
 DB 663 ATCAAGGTGCTGGGAACACCAACCCGGGAACAAATCCGAGAGATGAACCCCACTACAG 722
 QY 300 GluPheLysPheProGlnIleLysAlaHisProTyr-ThrLysValPheArgProArgTh 319
 DB 723 GAGTTCAAGTTCCCTCAGATTANAGCTCACCCCTGGGACAAAGGTGTCAAATCTCGAAC 782
 QY 319 rProProGluAlaIleAlaLeuCysSerArgLysLeuGluTyrThrProThrAlaArgLe 339
 DB 783 GCGGCGACAGGGCATCGGGCTCTGCTCTAGCCTGTGTGAGTACACCCCATCTCTCAGGCT 842
 QY 339 uThrProLeuGluAlaCysAlaHis-SerPhePheAsp 351
 DB 843 CTCCCCACTAGAAGGCTGTGGCAGACAGGCTTCTTTGAT 880

Search completed: September 18, 2006, 03:35:36
 Job time : 4638 secs